

GenCore version 4.5
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Om protein - protein search, using sw model

Run on: August 28, 2002, 17:31:49 ; Search time 20.26 Seconds
 Sequence: (without alignments)
 430.005 Million cell updates/sec

Title: US-09-502-984B-1
 Perfect score: 1194

BLOSUM62
 Gapop 10.0 , Gapext. 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_40; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1194	100.0	508	EPOR_HUMAN
2	982.5	82.3	507	EPOR_MOUSE
3	981.5	82.2	507	EPOR_RAT
4	205	17.2	625	TPOR_MOUSE
5	159	13.3	581	TPOR_HUMAN
6	151	12.6	581	TPR_BOVIN
7	148	12.4	616	TPR_CEREL
8	144.5	12.1	831	TPR_RABBIT
9	136.5	11.4	830	TPR_CHICK
10	135	11.3	831	TPR_COLI
11	128	10.7	622	TPR_MEGLA
12	126	10.6	119R_HUMAN	TPR_HUMAN
13	126	10.6	608	TPR_MOUSE
14	123.5	10.3	650	GHR_MOUSE
15	122.5	10.3	634	GHR_BOVIN
16	121	10.1	610	GHR_SHEEP
17	117.5	9.8	611	PRUR_RAT
18	117	9.8	638	GHR_COLI
19	117.5	9.8	1	GHR_PIG
20	117	9.8	608	GHR_CHICK
21	116.5	9.8	638	GHR_RABBIT
22	116.5	9.8	1	CYBR_HUMAN
23	116	9.7	897	PRUR_OREO
24	113	9.5	630	LIFR_HUMAN
25	111.5	9.3	1097	TLES_DROVI
26	108.5	9.1	638	GHR_RAT
27	108	9.0	976	EPA2_HUMAN
28	107	9.0	468	IL3R_MOUSE
29	106.5	8.9	378	113R_HUMAN
30	104.5	8.8	1165	LEPR_HUMAN
31	104	8.7	2594	TLES_DROVI
32	102	8.5	1	CYRB_MOUSE
33	101	8.5	977	EPA2_MOUSE

Scoring table: BLOSUM62

ALIGNMENTS

RESULT 1	EPOR_HUMAN	STANDARD;	PRT;	508 AA.
RN	ID EPOR_HUMAN			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=90304340; PubMed=2163696;			
RA	Jones S.S., D'Andrea A., Haines L.L., Wong G.G.; RT "Human erythropoietin receptor: cloning, expression, and biologic characterization.";			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Erythropoietin Receptor precursor (EPO-R).			
GN	EPO-R.			
RA	"The erythropoietin receptor gene: cloning and identification of multiple transcripts in an erythroid cell line OCML"; EXP. Hematol. 19:973-977(1991).			
RN	[2]			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=92399734; PubMed=1668606;			
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N., RT "Cloning of the human erythropoietin receptor gene.";			
RL	Kohkins W.D.; Blood 76:31-35(1990).			
RN	[3]			
RA	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta; MEDLINE=92399733; PubMed=1668606;			
RX	RC TISSUE=Placenta; MEDLINE=92399734; PubMed=1668607;			
RA	Macouche L., Tournamille C., Boffa G., Carttron J.P., RT "Cloning of the gene encoding the human erythropoietin receptor gene.";			
RA	Chretien S.; Blood 78:2546-2556(1991).			
RL	[4]			
RA	SEQUENCE OF 1-96 FROM N.A.			
RX	RC TISSUE=Placenta; MEDLINE=92399734; PubMed=1668607;			
RA	Macouche L., Tournamille C., Hattab C., Boffa G., Carttron J.P., RT "Cloning of the gene encoding the human erythropoietin receptor gene.";			
RA	Perry L.A., Forget B.G.; Blood 78:2546-2556(1991).			
RT	"Genomic organization of the human erythropoietin receptor gene.";			
RL	Genomics 11:974-980(1991).			
RN	[5]			
RP	SEQUENCE OF 1-17 FROM N.A.			
RX	MEDLINE=92147143; PubMed=1664413;			
RA	Perry L.A., Forget B.G.; Blood 78:2546-2556(1991).			
RT	"Genomic organization of the human erythropoietin receptor gene.";			
RL	Genomics 11:974-980(1991).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.			
RX	MEDLINE=96291992; PubMed=662230;			
RA	Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S., Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.; RT "Functional mimicry of a protein hormone by a peptide agonist: the EPO receptor complex at 2.8 A.;"			

RN	RL	SCIENCE 273:464-471(1996).
X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.	[7]	RX
MEDLINE=9903198; PubMed=980845;	RA	RA
Livnah O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,	RA	You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Pestka S.,
Jolliffe L.K., Wilson I.A.;	RA	Jolliffe L.K., Wilson I.A.;
"An antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation.";	RT	RT
Nat. Struct. Biol. 5:993-1004(1998).	RL	RN
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.	RX	RX
MEDLINE=9845092; PubMed=9774108;	RA	Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
Zhan H., Oslund T.D., Chirino A.J., Zhang J., Finer-Moore J., Wendoloski J.J.,	RA	Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
Egrie J., Stroud R.M.;	RA	CC
"Efficiency of signaling through cytokine receptors depends critically on receptor orientation.";	RT	RT
Nature 395:511-516(1998).	RL	RL
-1- FUNCTION: RECEPTOR FOR ERYTHROPOETIN. MAY PLAY A ROLE IN THE MECHANISM OF ERYTHROPOETIN-INDUCED ERYTHROBLAST PROLIFERATION AND DIFFERENTIATION.	[1]	RX
-1- SUBCELLULAR LOCATION: Type I membrane protein.	CC	CC
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	CC	CC
-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.	CC	CC
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DR EMBL: M34986; AAH52401.1; -.	DR	DR
DR EMBL: M460459; AAH52403.1; -.	DR	DR
DR EMBL: S45332; AAB3271.1; -.	DR	DR
DR EMBL: M76595; AAH52393.1; -.	DR	DR
DR EMBL: M77244; AAH52392.1; -.	DR	DR
PIR: AA3799; AA3799.	PIR	PIR
PIR: AA49824; AA49824.	PIR	PIR
PIR: A53958; A53958.	PIR	PIR
PDB: 1EFP; 29-JUL-97.	PDB	PDB
PDB: 1EBA; 18-NOV-98.	PDB	PDB
PDB: 1EER; 01-OCT-99.	PDB	PDB
PDB: 1ICN4; 11-AUG-99.	PDB	PDB
DR InterPro: IPR002996; CRLA.	DR	DR
DR InterPro: IPR03961; FNIII.	DR	DR
DR InterPro: IPR03528; Hematopo_receptor_L_FI.	DR	DR
Pfam: PF00041; fn3_1.	Pfam	Pfam
SMART: SM00660; FN3_1.	SMART	SMART
PROSITE: PS001352; HEMATOPO_REC_L_FI; 1.	PROSITE	PROSITE
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.	KW	KW
FT SIGNAL 1 24	FT	FT
FT CHAIN 25 508	FT	FT
FT DOMAIN 25 250	FT	FT
FT TRANSMEM 25 1 273	FT	FT
DOMAIN 148 508	FT	FT
DISULFID 52 62	FT	FT
CARBOHYD 91 107	FT	FT
SEQUENCE 508 AA; 508 AA;	SQ	SQ
Query Match 100.0%; Score 1194; DB 1; Length 508;	QY	QY
Best Local Similarity 100.0%; Pred. No. 7.3e-105; Indels 0; Gaps 0; Matches 225; Conservative 0; Mismatches 0;	QY	QY
APPNPNLDPDKFESKAALLAARGPPEELCFFTEREDIVCFWEENASAGVGPGWFSVQLE 60	QY	QY
61 DEPWKLCLHQATARGAVRFWSLPTADTSVPLERVTAAAGPAPHRVHNIEVL 120	Db	Db
144	RA	RA
DEPWKLCLHQATARGAVRFWSLPTADTSVPLERVTAAAGPAPHRVHNIEVL 144	RA	RA
121 LDAPVGLVARLADESQGHVLRWLWLPPEPMTSHTREYDVSAQNGAGSVQRVEILLEGRTE 180	QY	QY
204	QY	QY
145 LDAPVGLVARLADESQGHVLRWLWLPPEPMTSHTREYDVSAQNGAGSVQRVEILLEGRTE 204	Db	Db
181 CVLSNLNRGTRTRYFAVARMMAEFSGGFWSAWSEPVPSLTPSDID 225	QY	QY
249	Db	Db
205 CVLSNLNRGTRTRYFAVARMMAEFSGGFWSAWSEPVPSLTPSDID 249	QY	QY
RESULT 2	EPOR_MOUSE	EPOR_MOUSE
ID EPOR_MOUSE STANDARD; PRT; 507 AA.	ID	ID
AC P14753; Q63852; DT 01-APR-1990 (Rel. 14, Created)	AC	AC
DT 01-APR-1990 (Rel. 14, Last sequence update)	DT	DT
DE Erythropoietin receptor precursor (EPO-R).	DE	DE
GN EPOR.	GN	GN
OS Mus musculus (Mouse).	OS	OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC	OC
OX NCBI_TAXID=10090; RN [1]	OX	OX
RP SEQUENCE FROM N.A.	RP	RP
RX MEDLINE=8919238; PubMed=2539263; RA D'Andrea A.D., Lodish H.F., Wong G.G.; RT "Expression cloning of the murine erythropoietin receptor.";	RX	RX
Cell 57:277-285(1989).	RL	RL
RN [2]	RN	RN
RP SEQUENCE FROM N.A.	RP	RP
RX STRAIN=BALB/C; TISSUE=Liver;	RX	RX
DR MEDLINE=91080149; PubMed=2175360; RA Kuramochi S., Ikawa Y., Todokoro K.; RT "Characterization of murine erythropoietin receptor genes.";	DR	DR
DR MEDLINE=9217032; PubMed=1656233; RA Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.; RT "Unregulated expression of the erythropoietin receptor gene caused by insertion of spleen focus-forming virus long terminal repeat in a murine erythroblastoma cell line.";	DR	DR
DR MEDLINE=9217032; PubMed=1656233; RA Mol. Cell. Biol. 11:5527-5533(1991).	DR	DR
RN [14]	RN	RN
RP SEQUENCE OF 1-27 FROM N.A.	RP	RP
RX MEDLINE=90287158; PubMed=2162479; RA Yousoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.; RT "Structure and transcription of the mouse erythropoietin receptor gene.";	RX	RT
RT Mol. Cell. Biol. 10:3675-3682(1990).	RT	RT
RN [15]	RN	RN
RP SEQUENCE OF 1-24 FROM N.A.	RP	RP
RX MEDLINE=91201346; PubMed=1849897; RA Lacombe C., Chretien S., Lemarchandell V., Mayeux P., Romeo P.H., RA Gisselbrecht S., Cartron J.P.; RT "Spleen focus-forming virus long terminal repeat insertion in the T3C1-2 friend leukemia cell line.";	RX	RT
RT Mol. Cell. Biol. 13:1788-1795(1993).	RT	RT
J. Biol. Chem. 266:6952-6956(1991).	RL	RL
RN [16]	RN	RN
RP MUTAGENESIS.	RP	RP
RX MEDLINE=3180026; PubMed=8382775; RA Miura O., Cleveland J.L., Ihle J.N.; RT "Inactivation of erythropoietin receptor function by point mutations in a region having homology with other cytokine receptors.";	RX	RT
Mol. Cell. Biol. 13:1788-1795(1993).	RT	RT
-1- FUNCTION: RECEPTOR FOR ERYTHROPOETIN. MAY PLAY A ROLE IN THE	CC	CC

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CC DR EMBL; M90102; AAB69971.1; - .
 CC DR EMBL; M90103; AAB69972.1; - .
 CC DR EMBL; U68162; AAB08424.1; - .
 CC DR EMBL; U68159; AAB08424.1; JOINED.
 CC DR EMBL; U68160; AAB08424.1; JOINED.
 DR EMBL; U68161; AAB08424.1; JOINED.
 DR PIR; A45566; A45266.
 DR HSSP; P19235; 1EBA.
 DR MIM; 159330; - .
 DR MIM; 604498; - .
 DR InterPro; IPR00396; CRLA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003962; Hematopo_receptor_L_F1.
 DR PFAM; PF00041; fn3; 2.
 DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
 Repeat; Antigen; Polymorphism.
 PT SIGNAL 1 25
 FT CHAIN 26 635
 FT DOMAIN 26 491
 FT TRANSMEM 492 513
 FT DOMAIN 514 635
 FT DISUFRID 40 50
 FT DISUFRID 77 93
 FT DISUFRID 291 301
 FT DISUFRID 323 334
 FT CARBOHYD 117 117
 FT CARBOHYD 178 178
 FT CARBOHYD 298 298
 FT CARBOHYD 358 358
 FT VARSPLIC 523 579
 FT VARSPLIC 58 58
 FT VARSPLIC 168 168
 FT SEQUENCE 635 AA; 71244 MW; D25D8D8959359DDC CRC64;

Query Match 15.5%; Score 185; DB 1; Length 635;
 Best Local Similarity 24.5%; Pred. No. 9.4e-10;
 Matches 67; Conservative 30; Mismatches 117; Indels 60; Gaps 9;

QY 3 PPNLDPKFKFSKAALLAARGPEELICFTERLELDLVCFWEEAASAGVGPGNYSFSYOLED
 17 PQNL--AQVSSQDSVLLASDSEPLKCFSRFFEDLCFWDEEEAA - PSGTIQQLIAYPRE 62

QY 63 PWKLQRHLQOPTARGAVFCSLP-TADISSEPVPLRV-TAAGAPRHRVHINEVVL 120

Db 73 KPRACPLSSOSMMPHRGTRYVCQFPDOEVEYLFLPHLWYKVNLFNQTRVPLFVDSL 132

QY 121 LDAPVGLVARLADESQHVVLW-LPPPTPMTHRYEV---DVSAGNGAGSVORV- 173

Db 133 PAPPSIKANGGSGPGELOIISWEEAPE--ISDELRYLYRGPRPKNSGPPIVLIAT 190

QY 174 --TLEGRHECTVLSNLRG 189

Db 191 ETCCPALQRFHSASLDQSPCAQPTMPWQDGPKQTSPSREALTAEGGS-CLISGLQPG 249

QY 190 TRYTFAVRARMAPSFQGGWSAWBEPVSLITPSD 223

QY 250 NSYWIQLRREPDGTSIGGSGWSWSPVTVDLPGD 283

	RESULT	6	
PRLR_BOVIN	PRLR_BOVIN	STANDARD;	
ID	PRLR_BOVIN	PRT;	581 AA.
AC	Q28172;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	PROLactin receptor precursor (PRL-R).		
GN	PRLR		
OS	Bos taurus (Bovine).		
OC	Fukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Endometrium;		
RX	MEDLINE=9246019; PubMed=1338725;		
RA	Scott P., Ressier M.A., Schuler L.A.;		
RT	"Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues."		
RT	Mol. Cell. Endocrinol. 80:47-58(1992).		
RL	-I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.		
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.		
CC	-I- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1; 1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
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CC	DR InterPro; IPR003961; FN III.		
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CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
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CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
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CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
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CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
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CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
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CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
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CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
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CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		
CC	DR PFAM; PF00041; fn3; 2.		
CC	DR PROSITE; PS01352; HEMATOPREC_L_F1; 1.		
CC	DR InterPro; IPR00396; CRLA.		
CC	DR InterPro; IPR003961; FN III.		
CC	DR InterPro; IPR003962; Hematopo_receptor_L_F1.		

Matches	51:	Conservative	36:	Mismatches	100:	Indels	26:	Gaps	9:
QY	126	GLYARL--ADESHGVVLRWLPPLPPPTPMWSH--IRYEVDVSAGNGASVORLEGR 179							
Db	132	NLTILELKHPEDPKYLWIKWSPPTMDVSGWFITQYERILKPEKATDWTHFTLQ--T 189							
Qy	180	ECVLNLRCRTRRYFAVRARMAESFSGGWSAWEPVSILTPSD 223							
Db	190	QLKIFNLPQGKYIVQIRK--PDH-GYWSENPRESSIQIPND 229							
RESULT	7								
ID	PRL_CEREL	STANDARD:	PRT:	581 AA.					
OC	Q24235;								
DT	01-NOV-1997	(Rel. 35, created)							
DT	01-NOV-1997	(Rel. 35, last sequence update)							
DT	15-JUL-1998	(Rel. 36, last annotation update)							
DE	prolactin receptor precursor (PRL-R).								
GN	PRLR.								
OS	Cervus elaphus (Red deer)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi								
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; NCBI_TaxID=9860;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Liver;								
RA	MEDLINE=96030711; PubMed=7561644;								
RA	Clarke L.A., Ederry M., Loudon A.S., Randall V.A., Postel-Vinay M.C., Kelly P.A., Jabbour H.N.;								
RT	"Expression of the prolactin receptor gene during the breeding and non-breeding seasons in red deer (Cervus elaphus): evidence for the expression of two forms in the testis.";								
RT	J. Endocrinol. 146:313-321(1995).								
-i-	FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.								
CC	-i- SUBCELLULAR LOCATION: Type I membrane protein.								
CC	-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.								
CC	-i- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.								
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DR	EMBL; X94953; CAA64419.1; HSSP; P14787; LAN3; InterPro; IPR02996; CRLA.								
DR	InterPro; IPR03961; FN_III.								
DR	InterPro; IPR03528; Hematopo_receptor_L_F1.								
DR	Pfam; PF00041; fn3; 2.								
DR	SMART; SM00560; FN3; 1.								
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.								
DR	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.								
DR	SIGNAL 1 BY SIMILARITY.								
FT	PROLACTIN RECEPTOR.								
FT	DOMAIN 25 BY SIMILARITY.								
FT	EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEMBRANE 235 BY SIMILARITY.								
FT	POTENTIAL.								
FT	DOMAIN 259 BY SIMILARITY.								
FT	CYTOSLASMIC (POTENTIAL).								
FT	FIBRONECTIN TYPE-III 1.								
FT	DOMAIN 25 BY SIMILARITY.								
FT	FIBRONECTIN TYPE-III 2.								
FT	DISULFID 36 BY SIMILARITY.								
FT	DISULFID 75 BY SIMILARITY.								
FT	CARBONYD 59 BY SIMILARITY.								
FT	CARBONYD 132 BY SIMILARITY.								
FT	CARBONYD 233 BY SIMILARITY.								
SEQUENCE	SEQUENCE 581 AA; 65159 MW; 97547C963CP28EC CRC64;								
Query	12.6%	score 151;	DB 1;	Length 581;					
Match	Best Local Similarity	23.9%	Pred. No. 1.3e-06;						

FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 616 PROLACTIN RECEPTOR.
 FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 235 258 POTENTIAL.
 FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III 2.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 616 AA; 68840 MW; 800E3166FER7108C CRC64;

Query Match 12.4%; Score 148; DB 1; Length 616;
 Best Local Similarity 24.5%; Pred. No. 2.8e-05; Mismatches 103; Indels 42; Gaps 11; Matches 57; Conservative 31; MisMatches 103; Del 0; Insert 0; PRT; 616 AA.

Qy 3 PPNLPPKFESKAALLAARGPEELLCFTERLEDVCFWEAASAGVGPONYFSVQLEDE 62
 Db 27 PRGKP-----FIFKCRSPEK-----ETFCWWRGADGGL-PTNVLTHKEGE 69

Qy 63 PWKLCRHQAFTARGAVRFWCSLPLADTSSVTPLELRVTAAS-----GAPRYHRVHTN 116
 Db 70 ---TITHECFDYKIGGPNSCYFSKKHTSIWIIYIIVNATNQMGSSVSVDRY---VDVT 122

Qy 117 EVVLLDAVPVGI---VARLADSGHVLRLWLPPEPPTMS---HIRVEDVSAAGNGAGSVQ 170
 Db 123 YVVEPPPVNLTEVKHPEDKRPPVLYKWKLPVTLVDRSGWMLQFEIRAKPEKAA--EW 180

Qy 171 RVEILEGRTECVLSNLRGRRTYFAVRARMAEPFGFWSAWSPEVSLLTPSD 223
 Db 181 ETHFAQOQTOKFILSLYLGPGYLVQRC---PDH-GFWSTWSPESSIQIPND 229

RESULT 9
 PRLR_CHICK STANDARD; PRT; 831 AA.

ID PRLR_CHICK STANDARD; PRT; 831 AA.

AC 004594; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE prolactin receptor precursor (PRL-R) (CPRLP).

GN PRLR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. Gallus (Chicken).

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. Gallus (Chicken).

NCBI_TaxID=9031; RN [1] SEQUENCE FROM N.A.

RP STRAIN="WHITE LEGHORN"; TISSUE=Kidney; MEDLINE=93075121; PubMed=1445292;

RX RA Tanaka M., Maeda K., Okubo T., Nakashima K.; "Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence.", Biochem. Biophys. Res. Commun. 188:490-496(1992).

RL -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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DR EMBL; D13154; BAA02439.1; -.

DR PIR; J01655; JQ1655.
 DR HSPP; P14787; LAN3.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003528; Hematopo_receptor_L_F1.
 DR pfam; PF00041; fn3; 4.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831 PROLACTIN RECEPTOR.
 FT DOMAIN 24 438 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 326 428 FIBRONECTIN TYPE-III 2.
 FT DISULFID 36 459 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 460 459 FIBRONECTIN TYPE-III 4.
 FT CARBOHYD 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 BY SIMILARITY.
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADBB9 CRC64;

Query Match 12.1%; Score 144.5; DB 1; Length 831;
 Best Local Similarity 23.5%; Pred. No. 8.6e-05; Mismatches 103; Indels 43; Gaps 11; Matches 55; Conservative 33; MisMatches 103; Del 0; Insert 0; PRT; 831 AA.

Qy 3 PPNLPPKFESKAALLAARGPEELLCFTERLEDVCFWEAASAGVGPONYFSVQLEDE 62
 Db 230 PPEKP-----TIKCRSPEK-----ETFCWWRGADGGL-HPTNVTLYSKEGE 272

Qy 63 PWKLCRHQAFTARGAVRFWCSLPLADTSSVTPLELRVTAAS-----GAPRYHRVHTN 116
 Db 273 E---QVVECDYRAGPNSCYFDKHTSWMTWNIYTRATNEMGSNSPHY --VDVT 325

Qy 117 EVVLLDAVPVGI---VARLADSGHVLRLWLPPEPPTMS---HIRVEDVSAAGNGAGSVQ 170
 Db 326 YVVPDPNVNTLEKKPKNPYKVLWTWSPPPLADVRSGLTLEYLRKPEEGE--E 382

Qy 171 RVEILEGRTECVLSNLRGRRTYFAVRARMAEPFGFWSAWSPEVSLLTPSD 223
 Db 383 WETIFVGQOTOKMFSLNPGKYYIIOICK---PDHGSNWSSENNTQIOPND 433

RESULT 10
 PRLR_COLLI STANDARD; PRT; 830 AA.

ID PRLR_COLLI STANDARD; PRT; 830 AA.

AC 090374; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE prolactin receptor precursor (PRL-R).

GN PRLR.

OS Columba livia (Domestic Pigeon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba. NCBI_TaxID=8932; RN [1] SEQUENCE FROM N.A.

RP TISSUE=Cropsac;
 RC MEDLINE=94283267; PubMed=7516866;
 OC Chen X., Horserman N.D.; Chen "Cloning, expression, and mutational analysis of the Pigeon prolactin receptor.";

RL Endocrinology 135: 269-276(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL; U07634; AAA20646; 1; -.
 DR InterPro; IPR0052996; CRLA.
 DR InterPro; IPR0052961; FN_III.
 DR InterPro; IPR0052952; Hematopo_receptor_L_F1.
 DR SMART; SM00060; FN3; 4.
 PROSITE; P501352; HEMATOPO_REC_L_F1; 1;
 Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 25 122
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 SQ SEQUENCE 830 AA; 94507 MW; 3B074E83CD69EFF CRC64;

Query Match Score 11.4%; DB 1; Length 830;
 Best Local Similarity 23.2%; Pred. No. 4 9e-05; Indels 45; Gaps 11;
 Matches 55; Conservative 3; Mismatches 104; Indels 45; Gaps 11;

OY 4 PNLPDKFKEFKAALLAARGPPEELCFTERLEDLVCWEEAASAGVPGNTSFYQLEDEP 63
 Db 226 PNGESP--PERKPTIKRSPEK-----EDTCWKKPGSDGG-HPTNYTLYSKREEE 274
 OY 64 WKLCLRHQAAPTARGAYRFWCSLPTADTSFVPLERLVTAAS-----GAPRYHRVTHINE 117
 OY 275 ---RVECPDYKTAGPNSCFDKKTFSFWTIINTVKATNEIGNSVSDPLY--WDVTY 327
 OY 118 VVLLDAVPGVYLRL---ADESGHVVWRWLPPETPMs--HIRYEVDSAGNGAGSWQR 171
 Db 328 IVQTDPBPVNVLLEKKTKVNRPKVLYLTWSPPPLADYRSGLWLTDLRLK-----EE 380
 OY 172 VEILE----GRTECVLSNLRRTRTFAVARMAEPSEFGGEWSAMSEPSVSLTPSD 223
 Db 381 AEEWETLFVGQOTHYKMFSLNPKKYIWOHCK--PDHGWSWENSLEKLOIPD 434

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (tPRLR).
 GN PRLR.
 OC Meleagris gallopavo (Common turkey);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OC NCBI_TaxID:9103;
 RN [1]
 RP TISSUE-Kidney;
 RC Zhou J.-F., Zadworny D., Guemene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallipavo.";
 RL Biol. Reprod. 55:1081-1090(1996).
 RN [2]
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE-Ovary;
 RA Pitts G.R., You S.K., Foster D.N., el Halawani M.F.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC DR EMBL; L76587; ARB0154; 1; -.
 DR EMBL; U22947; AAA75038; 1; -.
 DR EMBL; U22934; AAA75039; 1; -.
 DR HSSP; R16471; 1BP3.
 DR InterPro; IPR002896; CRLA.
 DR InterPro; IPR0052961; FN_III.
 DR InterPro; IPR0052952; Hematopo_receptor_L_F1.
 DR SMART; SM00060; FN3; 3.
 PROSITE; P501352; HEMATOPO_REC_L_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438
 FT TRANSMEM 439 459
 FT DOMAIN 460 831
 FT DOMAIN 25 122
 FT DOMAIN 123 225
 FT DOMAIN 228 325
 FT DOMAIN 326 428
 FT DISULFID 336 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT CARBOHYD 315 315
 FT CARBOHYD 335 335
 SQ SEQUENCE 831 AA; 94394 MW; 220916320F7FA1 CRC64;

Query Match Score 11.3%; DB 1; Length 831;
 Best Local Similarity 22.9%; Pred. No. 6 7e-05; Indels 20; Gaps 7;
 Matches 48; Conservative 36; Mismatches 106; Indels 20; Gaps 7;

RESULT 11
 PRLR_MELGA
 ID_PRLR_MELGA STANDARD; PRT; 831 AA.
 AC 091094; 091091; 091092;
 DT 01-NOV-1997 (Rel. 35, Created)

23 PEEELCFTERLEDIVCFWEREASAGVGGVGSFSYQLEDEPWKLCLRHOAPTARGAVREW 82
 CC or send an email to license@ib-sib.ch).

Db 31 PKIIRCRSLERKETFSCWKPGSDGGL-PTNLYTFLSKDSE---KIVECPDYRTSGPNS 85
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ib-sib.ch/announce/>
 CC

DR EMBL: M31661; AAS0174_1; -.

DR EMBL: AF091870; AAD32032_1; JOINED.

DR EMBL: AF091863; AAD32032_1; JOINED.

DR EMBL: AF091864; AAD32032_1; JOINED.

DR EMBL: AF091865; AAD32032_1; JOINED.

DR EMBL: AF091866; AAD32032_1; JOINED.

DR EMBL: AF091867; AAD32032_1; JOINED.

DR EMBL: AF091868; AAD32032_1; JOINED.

DR EMBL: AF091869; AAD32032_1; JOINED.

DR EMBL: AF349939; AAK32703_1; -.

DR PIR: A40144; A40144.

DR PDB: 1B93; 23-SEP-98.

DR MIH: 176761; -.

DR InterPro: IPR02996; CRIA.

DR InterPro: IPR03961; FN_III.

DR InterPro: IPR03538; Hematopo_receptor_L_F1.

DR Pfam: PF0041; fn3; 2.

DR SMART: SM00050; FN3; 1.

DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;

KW Alternative splicing; 3D-structure.

FT SIGNAL 1 24 PROLACTIN RECEPTOR.

FT CHAIN 25 622 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 25 234 POTENTIAL.

FT TRANSMEM 235 258 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 622 FIBRONECTIN TYPE-III 1.

FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.

FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VANSPLIC 233 233 MISSING (IN ISOFORM 2).

FT SEQUENCE 622 AA; 69505 MN; DB7FD032860BC787 CRC64;

Query Match 10.7%; Score 128; DB 1; Length 622;
 Best Local Similarity 23.8%; Pred. No. 0.00021;
 Matches 50; Conservative 33; Mismatches 107; Indels 20; Gaps 9;

RT "The human prolactin receptor gene structure and alternative promoter
 utilization: the generic promoter hPRII and a novel human promoter
 hP(N)." ;

RT J. Clin. Endocrinol. Metab. 84:1153-1156(1999).

RT [3]

SEQUENCE FROM N.A. (ISOFORM 2).

RT TISSUE=Breast carcinoma;

RT Kline J.B., Cleverger C.V.;"

RT "Characterization of a novel and functional human prolactin receptor
 isoform (delta-S1 PRL) containing only one extracellular
 fibronectin-like domain.";

RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RT [4]

RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-335.

RX MEDLINE-9507562; PubMed-7984244;

RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;

RT "The x-ray structure of a growth hormone-prolactin receptor complex.";

RT Nature 372:478-481(1994).

RT -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 2 Isoforms; 1 (shown here) and 2/delta-S1;
 are produced by alternative splicing.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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RESULT 13

ILQR_HUMAN STANDARD; PRT; 522 AA.

QY 23 PEEELCFTERLEDIVCFWEREASAGVGGVGSFSYQLEDEPWKLCLRHOAPTARGAVREW 82
 Db 31 PEIFKCRSPNPKERTCWRPGTUGGL-PTNLYTFLSKDSE---KIVECPDYRTSGPNS 85

QY 83 CSLPTADISSFVPLRLTAAS-GAPRVHRV-TIINEVLLDAPVGL---VARLADSG 136
 Db 86 CHFGKQYTSMWR3YIMMVNATNOMGSSFSDLVXDVNTIVQDPPLALEAVEVKOPEDRKP 145

QY 137 HVVLRLWLPPETMTS---HIREVDVAGNGAGSVQRVEILSGRTCEVLSNRGRRTRT 193
 Db 146 YLMWIKWSPEPLDILKTGWNFLYLIERLKPEKAA--EWEIHFAQOQTTEFKILSLHPQKYL 203

QY 194 FAVRARMAEPSPFGFWSAWSEPYVLSSLTSD 223
 Db 204 VQVRCK---PDH-GYWSAWSPATFQIQFSD 229

RN	NCBI_TaxID=9605;
[1]	SEQUENCE FROM N.A.
RX	MEDLINE=92302307; PubMed=1376929;
RA	Renauld J.C., Bruez C., Kermouni A., Houssiau F., Uyttenhove C., van Roost E., van Snick J.;
RA	"Expression cloning of the murine and human interleukin 9 receptor genes.";
RT	Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694(1992).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94250901; PubMed=8193355;
RA	Chang M.S., Engel G., Benedict C., Basu R., McNinch J.;
RA	"Isolation and characterization of the human interleukin-9 receptor gene";
RT	Blood 83:3199-3205(1994).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Melanoma;
RX	MEDLINE=96115587; PubMed=8666384;
RA	Kermouni A., van Roost E., Arden K.C., Vermeesch J.R., Weiss S., Godelain D., Flint J., Lurquin C., Szikora J.P., Higgs D.R., Marlyn P., Renauld J.C.;
RA	"The IL-9 receptor gene (IL9R): genomic structure, chromosomal localization in the pseudautosomal region of the long arm of the sex chromosomes, and identification of IL9R pseudogenes at 9qter, 10pter, 16pter, and 18pter.;"
RL	Genomics 26:371-382(1995).
-I-	FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-9.
-I-	SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.
CC	-I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC	-I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC	-----
DR	EMBL: M84747; AAA58679_1; -
DR	EMBL: S71404; ARB30844_2; ALT_SEQ.
DR	EMBL: S71420; AAD14081_1; -
DR	EMBL: L39064; AAC29513_1; -
DR	PIR: BA5268; BA5268.
DR	MM: 300007; -
DR	InterPro: IPR002996; C1A.
DR	InterPro: IPR03531; Hematopo_receptor_S_F1.
DR	InterPro: IPR03531; HEMATOPO_REC_S_F1; 1.
KW	Receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 40 POTENTIAL.
FT	CHAIN 1 40 INTERLEUKIN-9 RECEPTOR.
FT	DOMAIN 41 270 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 271 291 POTENTIAL.
FT	DOMAIN 292 522 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 150 244 FIBRONECTIN TYPE-III.
FT	DOMAIN 429 439 POLY-SER.
FT	DOMAIN 440 443 POLY-ASN.
FT	CARBOHD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT 331 331 R->G (IN REF. 3).
FT	CONFLICT 439 439 MISSING (IN REF. 3).
SEQUENCE	522 AA; 57333 MW; E6CB5C6342DE2BB2 CRC64;
Query Match	10.6%; Score 126; DB 1; Length 522;
Best Local Similarity	24.6%; Pred. No. 0_00027;
Matches	58; Conservative 25; Mismatches 93; Index 60; Gaps 13;
OY	21 RGPEE--LLCTTEREDIVCFNEEAASAGVGGNYSFSVQLEDPWKLRCHQAP----- 73
• : : : : : : : : :	
RESULT	14
PRLR_MOUSE	STANDARD;
ID	PRL_MOUSE
AC	Q00501; Q62099; P15213; P15212;
RC	01-APR-1990 (Rel. 14, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Prolactin receptor precursor (PRL-R).
GN	PRL-R
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (FORM PRL-R3).
RC	STRAIN=C3H; TISSUE= Mammary gland;
RC	MEDLINE=94065788; PubMed=8202385;
RA	Moore R.C., Oka T.;
RA	"Cloning and sequencing of the cDNA encoding the murine mammary gland long form prolactin receptor.;"
RL	Gene 134:263-265(1993).
RN	[2]
RP	SEQUENCE FROM N.A. (FORM PRL-R3).
RC	STRAIN=SWISS WEBSTER; TISSUE=Liver;
RC	MEDLINE=93301749; PubMed=8319571;
RA	Clarke D.L., Linzer D.T.H.;
RA	"Changes in prolactin receptor expression during pregnancy in the mouse ovary.";
RL	Endocrinology 133:224-232(1993).
RN	[3]
RP	SEQUENCE FROM N.A. (FORM PRL-R3).
RA	Sasaki M.;
RA	Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RL	Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A. (FORM PRL-R3).
RC	STRAIN=BALB/C; TISSUE=Mammary gland;
RA	Edery M., Pezet A., Nandi S., Kelly P.A.;
RA	Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
RC	STRAIN=SWISS WEBSTER; TISSUE=Liver;
RC	MEDLINE=89261824; PubMed=2725531;
RA	Davis J.A., Linzer D.I.H.;
RA	Expression of multiple forms of the prolactin receptor in mouse liver.;"
RT	Mol. Endocrinol. 3:674-680(1989).
RL	-----
CC	-I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN AS WELL AS PLACENTAL LACTOGEN I AND II.
CC	-I- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC	-I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; PRL-R1, PRL-R2 AND PRL-R3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPlicing.
CC	-I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC	-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC EMBL; LI3593; AAC37641.1; -.

DR EMBL; D1021; BAA01066.1; -.

DR EMBL; X73372; CAA5189.1; -.

DR EMBL; M22959; AAA39977.1; -.

DR EMBL; M22958; AAA39976.1; -.

PIR; JTO671; JTO671.

HSSP; P1478; IAN3.

MGD; MGI:9773; PRL.

DR InterPro; IPR002996; CRLA.

DR InterPro; IPR003961; FN_ITI.

DR Pfam; PF00041; In3; 2.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;

KW Alternative splicing

FT SIGNAL 1 19

FT DOMAIN 20 608

FT TRANSMEM 230 253

FT DOMAIN 254 608

FT DOMAIN 20 117

FT DOMAIN 119 222

FT DISULFID 31 41

FT DISULFID 70 81

FT CARBOHYD 54 54

FT CARBOHYD 99 99

FT CARBOHYD 127 127

FT VARSPLIC 281 292

FT VARSPLIC 293 608

FT VARSPLIC 304 608

FT VARSPLIC 558 558

FT CONFLICT 608 AA; 68240 MW; B8C2B2B2EFC9FC6 CRC64;

SQ

Query Match 10.6%; Score 126; DB 1; Length 608;

Best Local Similarity 22.3%; Pred. No. 0; 0.0033; Matches 47; Conservative 38; Mismatches 104; Indels 22; Gaps 8;

Qy 23 PEEELCFTERIEDLYCWEEAASAGVGPGNFSYKOLEDEPWKLCLRHQAFTARGAVRFW 82

Db 26 PEIKHORSPDKETFCWQWNPCSDGGL-PTNVSLSITSKEGER--NTYEPDYKTSGPNS 80

Qy 83 CSPLTADTSSVPLELRVTA---ASGAPYHRVHTINEWVLLDAPVGL--VARLAD 133

Db 81 CFFSKOVTISWKKIYTIVNATNEMGSTSDSLPH--DVDTYIVVEPPPRNLTEVKQLKD 137

Qy 134 ESGHVWLRLPPEPM-TSHIRVEVDASAGNGGSVQRVLELEGRTECVLSNRGRTRY 192

Db 138 KRTYLVWKWLPPPTIDVKTGWTMEEYIRLKSEADEWEIHFTHQTOFKVFDLYPGQKY 197

Qy 193 TFAVRKRMAEPSFGGWSANSEPVSLTPSD 223

Db 198 LWQTRECK---PDH-GYWSRWGQEKSIEIPND 224

RESULT 15

GHR_MOUSE STANDARD; PRT; 650 AA.

ID 16892; P16590; ORP264;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (GH binding protein) (GBBP) (serum binding protein).

GN GHR.

OS mus musculus (Mouse).

OC Fukkaroata; Metacora; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX MEDLINE=8925449; PubMed=2739661;

RX MEDLINE=99367316; PubMed=1042545;

RX Moffat J.G., Talamantes F.; "Mouse serum growth hormone (GH) binding protein has GH receptor extracellular and substituted transmembrane domains." Mol. Endocrinol. 3:994-990(1989).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX STRAIN=Swiss Webster, and DBA/J;

RX SEQUENCE FROM N.A. (ISOFORM 2).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX STRAIN=Swiss Webster, and DBA/J;

RX STRAIN=C57BL;

RX "Mouse growth hormone receptor/binding protein and growth hormone receptor transcripts are produced from a single gene by alternative splicing." J. Mol. Endocrinol. 23:33-44(1999).

RX STRAIN=Swiss Webster, and DBA/J;

RX STRAIN=C57BL;

RX MEDLINE=95201642; PubMed=7984338;

RX Zhou Y., He L., Kopchick J.J.; "An exon encoding the mouse growth hormone binding protein (mGHBp) carboxy terminus is located between exon 7 and 8 of the mouse growth hormone receptor gene." J. Mol. Endocrinol. 103:223-227(1994).

RN [4]

RP SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).

RX STRAIN=C57BL;

RX MEDLINE=95201642; PubMed=7984338;

RX Zhou Y., He L., Kopchick J.J.; "An exon encoding the mouse growth hormone receptor gene." J. Mol. Endocrinol. 103:223-227(1994).

RN [5]

RP REVISTONS.

RC STRAIN=CS7BL;

RA Zhou Y., He L., Kopchick J.J.; "An exon encoding the mouse growth hormone receptor gene." J. Mol. Endocrinol. 103:223-227(1994).

RN [6]

RP Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

RP SEQUENCE OF 25-41.

RX MEDLINE=88288223; PubMed=3398846;

RA Smith W.C., Colosi P., Talamantes F.; "Isolation of two molecular weight variants of the mouse growth hormone receptor." Mol. Endocrinol. 2:108-116(1988).

CC -I- FUNCTION: Isoform 1 is a receptor for pituitary gland growth hormone. Isoform 2 is a serum growth hormone binding protein that may play an important role in regulating the effective serum concentration of gh.

CC -I- SUBUNIT: Isoform 1 is a homodimer.

CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); secreted (isoform 2).

CC -I- ALTERNATIVE PRODUCTS: 2 isoforms: 1/LMW GHR (shown here) and 2/LMW GHR; are produced by alternative splicing.

CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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CC

DR EMBL; M3334; AAA37690.1; ALT-SEQ.

DR EMBL; M31680; AAA37889.1; ALT-SEQ.

DR EMBL; AF120481; AAD32556.1; JOINED.
 DR EMBL; AF120482; AAD32556.1; JOINED.
 DR EMBL; AF120483; AAD32556.1; JOINED.
 DR EMBL; AF120484; AAD32556.1; JOINED.
 DR EMBL; AF120485; AAD32556.1; JOINED.
 DR EMBL; AF120486; AAD32556.1; JOINED.
 DR EMBL; AF120487; AAD32556.1; JOINED.
 DR EMBL; AF120488; AAD32556.1; JOINED.
 DR EMBL; AF120487; AAD32555.1; -.
 DR EMBL; AF120481; AAD32555.1; JOINED.
 DR EMBL; AF120482; AAD32555.1; JOINED.
 DR EMBL; AF120483; AAD32555.1; JOINED.
 DR EMBL; AF120484; AAD32555.1; JOINED.
 DR EMBL; AF120485; AAD32555.1; JOINED.
 DR EMBL; AF120486; AAD32555.1; JOINED.
 DR EMBL; U49266; AAK62802.1; -.
 DR EMBL; U49268; AAK62802.1; JOINED.
 DR EMBL; U43933; AAK62802.1; JOINED.
 DR HSSP; P10912; IWHH.
 DR MGI; MGI-95708; Ghr.
 DR InterPro; IPR002896; CRLA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR00528; Hematopo_receptor_L_F1.
 DR PIam; PF00041; fn3; 1.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; signal; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 650 GROWTH HORMONE RECEPTOR.
 FT DOMAIN 25 273 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 274 297 POTENTIAL.
 FT DOMAIN 298 650 CYTOSOLIC (POTENTIAL).
 FT DOMAIN 153 260 FIBRONECTIN TYPE-III.
 FT DISULFID 56 66 BY SIMILARITY.
 FT DISULFID 109 120 BY SIMILARITY.
 FT DISULFID 134 148 BY SIMILARITY.
 FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 271 296 D1QFPWFLLTIGIFGVAVMLFWVIF->GKRSNSOHPHQ
 FT VARSPLIC 297 650 MISSING (IN ISOFORM 2).
 FT CONFLICT 25 T -> A (IN REF. 6).
 FT CONFLICT 162 162 T -> A (IN REF. 3 AND 4).
 FT CONFLICT 325 325 G -> E (IN REF. 2).
 FT CONFLICT 423 423 R -> A (IN REF. 2).
 SQ SEQUENCE 650 AA; 72783 MW; 95653380CAF0B931 CRC64;

Query Match 10.3%; Score 123.5; DB 1; Length 650;
 Best Local Similarity 22.6%; Pred. No. 0.0006; Indels 51; Gaps 10;
 Matches 52; Conservative 39; Mismatches 88; Indels 51; Gaps 10;

Oy 23 PBEELCFTERLIDLVCEWEEASAGY-GPGNWSFSYQLED-----EPWKLCLR 68
 Db 51 PRFTKCRSPELETFSCYWTGDNPDLKTPGSQLYYAKRESQRQARIAHETWQENKEC- 109

Oy 69 LHQCA¹PTARGAVRFWCSLPTADTSFPLERLRVTAASGAPRHRVHINEVILDAPVGLV 128
 Db 110 ---PDVVSAGRNCSCTFNSYVSIWIPYC¹KIT-TNGDLQCKFTYDEIWTQPPDPPIGLN 164

Oy 129 ARLADES-----GHVVLRLWPPEPETPMH---IRYEVDSAGANGAGSVQRVTELGR-- 178
 Db 165 WTLMLNLSLTGIRDQDIQWSQWPPPNADVLKGWITLEYF-----IQYKEVNESKW 213

Oy 179 -----TECVISNLRRRTYVFAVRARMAPEFGFWMSAMSEPVSLTIP 221

Oy 214 VMGPIWLTYCPVYSLRMDEKEHEVVRVSR--ORSFEKY-SEFSEVLRVIFP 260